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Minimum DB
Maximum DB
                                                                                                                                                                                  Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on:
  Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  141
133.5
132.5
129
129
127
127
                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 SPTREMBL_17:*

1: sp_archea:*
2: sp_bacteria:
3: sp_fung1:*
4: sp_human:*
5: sp_invertebr:
                                                                                                                                                                                  Query
Match
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11:
12:
13:
14:
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269
1 LARAGFYYIGPGDF
 Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LARAGEYYIGPGDRVACFAC.....WEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                              sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                   sp_invertebrate: *
                                                                                                                                                                                                                                                                                                                                                                              sp_bacteria:*
                                                                                                                                                                                                                                                                                  sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                                   sp_vertebrate;*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                      sp_plant:*
                                                                                                                                                                                   Length
  1140
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Q9ESE8
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Q9IA69
Q9IA69
Q88642
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Q9ESF0
Q9ESF0
Q9EQ05
Q9EQ05
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                Ogunhi homo sapien
Qogze6 rattus norv
Qogese8 rattus norv
Qogese9 rattus norv
Qoja60 gallus gall
Qoja60 gallus gall
Qoja60 gallus gall
Qogenfo rattus norv
Qogenfo mus musculu
Qoyenfo masacta moo
Qoyunz drosophila
Qogenfo ratsanoo
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 sapien
sapien
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4 5	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	82	27	93	25	24	23	22	21	20	
65	66.5	70.5	72	72	80	80	85.5	87.5	92	97	96	99.5	101.5	107	111	115.5	117	123	123	123	123	123	125	126	126	
24.2	24.7	26.2	26.8	26.8	29.7	29.7	31.8	32.5	34.2	36.1	36.4	37.0	37.7	39.8	41.3	12.9	43.5	45.7	45.7	45.7	45.7	45.7	46.5	46.8	46.8	
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009119 mus musculu	Q9yvk0 melanoplus	Q9bvz4 homo sapien	Q9j849 spodoptera	Q22837 caenorhabdi	Q9pz54 trichoplusi	092435 bombyx mori	09pyg9 xestia c-ni	ascoviru	Q9yk15 epiphyas po		092394 bombyx mori	Q9ddk0 gallus gall		ယ	Q9yvj4 melanoplus	Q9vh01 drosophila	O55770 chilo iride	Q9nj07 spodoptera	Q9j827 spodoptera	Q9ynl8 choristoneu	Q9ifi8 helicoverpa		O89744 buzura supp	Q9u492 trichoplusi	Q9qes9 epiphyas po	

ALIGNMENTS

OSUNNII OSUNNII DI ORTHI PRELIMINARY; PRT; 1140 AA. AC OSUNHII; DT 01-MAY-2000 (TYEMBLIE1 13, Created) DT 01-MAY-2000 (TYEMBLIE1 17, Last sequence update) DT 01-MAY-2000 (TYEMBLIE1 17, Last sequence update) DT 01-MAY-2000 (TYEMBLIE1 17, Last sequence update) DE APIZ-MLT FUSION PROTEIN. OC ENALTYOLD; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. OX NOBL_TAXID-9606; RN [1] RN MEDILINE-9272400; PubMed-10339464; RX MEDILINE-927240; PubMed-103394; RX MEDILINE-927240; RX MINTERPOORTER (SCASPASE) RX MEDILINE-927240; RX MEDI

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Matches

Inhibitor

of.

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Interpro: IPR001330; BIR.
Interpro: IPR001315; CARD.
Interpro: IPR001841; Znf_ring.
Interpro: IPR001841; Znf_ring.
Interpro: IPR001941; Znf_ring.
Pfam: PF00653; BIR; 3.
Pfam: PF00097; zf-C3HC4; 1.
SMART; SM00198; BIR; 3.
SMART; SM00114; CARD: 1.
SMART; SM00114; CARD: 1.
SMART; SM00114; RING: 1.
SMART; SM00114; RING: 1.
PROSITE: PS01282; BIR_REPEAT_1; 3.
PROSITE: PS01203; BIR_REPEAT_2; 3.
PROSITE: PS50209; CARD: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OSESE8
OSESE8
OSESE8
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPPOSIS PROTEIN 2.
ENARYOTOS (Rat),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae,
HCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9QZC6 PRELIMINARY; PRT; 589 AA.
Q9QZC6;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
SEQUENCE FROM N.A.
Holcik M., Lefebvre C.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 90.3%;
l Similarity 87.0%;
40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 91...
                                                                                                                                                                                                                                                                                                                                                                                         589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           66777 MW;
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91.3%;
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   Hicks
                                                                                                                                                                                                                                                                                                              ; Score 243; DB
; Pred. No. 7.4e
3; Mismatches
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Pred.
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                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                           E6812FFE3EA34142 CRC64;
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                                                                                                                                                                                                                                                                                                                               243; DB 11;
No. 7.4e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248; DB 4;
No. 3.3e-23
   Korneluk
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Best Local S
Matches 39
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Best Local S
Matches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF0063; BIR; 3.
Pfam; PF0063; CARD; 1.
Pfam; PF00097; Zf-C3BC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00184; RING; 1.
SMART; SM0184; RING; 1.
PROSITE: PS01282; BIR_REPEAT_1; 1.
PROSITE: PS0143; BIR_REPEAT_2; 3.
PROSITE: PS0143; BIR_REPEAT_2; 3.
PROSITE: PS0143; BIR_REPEAT_2; 3.
PROSITE: PS0143; BIR_REPEAT_2; 3.
                                                                                                                                                                                                         Pfam; PF00653; BIR; 3.
Pfam; PF00619; CARD; 1.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00114; CARD; 1.
SMART; SM00114; RING; 1.
SMART; SM001184; RING; 1.
                                                                                                                                                                                                                                                                                            Holcik M., Lefebyre C.A., Hicks K., Korneluk R.G.;
"Cloning and Characterization of the Rat Homologs of the
Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases
1- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL; ARF183430; AAG22990.1;
InterPro; IPR001370; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR0013841; Znf_ring.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ESE9 PRELIMINARY; PRT; 602 AA.
Q9ESE9; OPERATOR OF APOPTOSIS PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and Characterization of the Rat Homologs of the Apoptosis Protein 1, 2, and 3 Genes.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-: SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
EMBL, AF183431; AAG22971.1; -.
InterPro, IPR001379; BIR.
InterPro; IPR001315; CARD.
InterPro; IPR001315; CARD.
InterPro; IPR0013841; Znf_ring.
                                                                                                                                     PROSITE; PS01282; BIR_REPEAT_1;
PROSITE; PS50143; BIR_REPEAT_2;
PROSITE; PS50209; CARD; 1.
Zinc-finger.
SEQUENCE 602 AA; 67326 MW; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                  1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
   LAKAGFYYTGPGDRVACFACGGKLSNWDRKDDPLSEHRRHFPSCPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                             1 Similarity
39; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 589 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66750 MW;
                                                                         87.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.38;
                                                          Score 236; DB
Pred. No. 5.9e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 243; DB 11;
Pred. No. 7.4e-23;
3; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B4F7089BD7CD285B CRC64;
                                                                                                                                      CC91385EEA62DE5A CRC64;
                                                                         236;
No. 5.
                                                                                        Length
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   234
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Query Match Best Local S Matches 40

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Best Local S
Matches 37
                                                                                           STRAIN-BREED FAYOUMI; TISSUE-SPLEEN;
Zhou H., Lamont S.J.;
"CenetLe variation among chicken lines and mammalian species
specific genes.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF221083; AB753320.1;
InterPro; IPR001370; BIR.
Pfam; PF00653; BIR; 2.
SMART; SMO0238; BIR; 2.
PROSITE; PS01282; BIR_REPEAT_1; 2.
PROSITE; PS0143; BIR_REPEAT_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
PROSITE;
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SEQUENCE
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01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
1NHIBITOR OF APOPYOSIS I (FRACMENT).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-CCT-2000 (TrEMBLrel. 15, Created)
01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-CCT-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS 1 (FRAGMENT).
Gallus gallus (Chicken).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BREED LEGHORN; TISSUE-SPLEEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhou H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tted (JAN-2000) to the EMBL/GenBank/DDBJ databases AF221082; AAF35319.1; --
PFO: IPR001370; BIR.
PF00653; BIR; 2.
; SM00238; BIR; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity 80.4
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lamont S.J.; variation among chicken lines and mammalian species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS01282; BIR_REPEAT_1;
PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195
195 /
    197
197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑĄ.
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195
22347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae.
22602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 228; DB 1
Pred. No. 2e-21;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9C39BFA755E24E48 CRC64;
D7923DABCF623E1A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95
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RESULT
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Q9DDN2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR Pfam; PF00653; BIR; 2.

SMART; SM00238; BIR; 2.

PROSITE: PS50143; BIR REPEAT_2; 3

R NON_TER 1 1

NON_TER 224

SEQUENCE 224*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 37
Pendleton C.N., Bargmann W.J., Varadarajan J., B

"The apoptosis inhibitor ch-IAP1 is a direct trantive and c-rel,";

1 v-Rel and c-rel,";

1 Submitted (CCT-2000) to the EMBL/GenBank/DDBJ da EMBL, AF311289; AAA42316.1;

2 EMBL, AF311289; AAA42316.1;

R Ffam; PF00653; BIR; 3.

R Pfam; PF00653; BIR; 3.

R SMART; SM00238; BIR; 3.

R PROSITE; PS01282; BIR_REPEAT_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                         OSDDN2
PRELIMINARY;
PR
OSDNN2:
OI-MAR-2001 (TrEMBLrel. 16, Crea
OI-MAR-2001 (TrEMBLrel. 16, Last
OI-JUN-2001 (TrEMBLrel. 17, Last
APOPTOSIS INHIBITOR CH-IAP1 (FRA
Gallus gallus (Chicken).
Eukaryotta; Metazoa; Chordata; Cr
Archosauria; Aves; Neognathae; Gr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN-HISTAR; TISSUE-OVARY, CORPUS LUTEUM;

STRAIN-HISTAR; TISSUE-OVARY, CORPUS LUTEUM;

Bradley C.K., Lareu R.E., Dharmarajan A.M.;

"Cloning and characterisation of an inhibitor

"Cloning and characterisation" of an i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridee; Murinee; Rattus.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
hes 37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51
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nes 37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84.8%;
llarity 80.4%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.8%;
                                                                                                                                                                                                                                                      W.J., Varadarajan J., Bose H.R. Jr.; ch-IAP1 is a direct transcriptional target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
(FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 228; DB 11;
Pred. No. 2.3e-21;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213A52534D5EB56A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ≥ 228; DB 13
. No. 2e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                              of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Best Local S
Matches 37
                                                                                       InterPro: IPR001370; BIR.
InterPro: IPR001315; CARD.
InterPro: IPR001315; CARD.
InterPro: IPR001841; Znf_ring.
Pfam: PF00619; CARD.
Pfam: PF00619; CARD.
Pfam: PF00097; zf-C3HG4; 1.
SMART; SM00134; CARD. 1.
SMART; SM00114; CARD. 1.
SMART; SM00114; CARD. 1.
SMART; SM00184; RING; 1.
PROSITE; PS01282; BIR, REPEAT_1; 3.
PROSITE; PS01283; BIR, REPEAT_2; 3.
PROSITE; PS01283; BIR, REPEAT_2; 3.
PROSITE; PS012809; CARD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-WHITE LEGIONN; TISSUE-EMBRYONIC FIBROBLAST;

STRAIN-WHITE LEGIONN; TISSUE-EMBRYONIC FIBROBLAST;

MEDIJINE-98038801; Pubmed-9372964;

MI, KU P.-T., Hrdlickova R., Bose H.R. Jr.;

"Ch-IAPI, a member of the inhibitor-of-apoptosis protein family, is a mediator of the antiapoptotic activity of the v-Rel oncoprotein.";

MOI Cell. Biol. 17:7328-7341(1997).

-1- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED
REPEAT
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                      -)- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC EMBL; AF008592; AAB88044.1; -. HSSP; Q13490; 1QBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gallus gallus (Chicken).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS
                                                                                                                                                                                                                                                                                                                                   -I- DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
-I- SIMILARITY: MEMBER OF THE IAP FAMILY.
-I- SIMILARITY: COMPAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  057319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 LAKAGLYYLGTADKVACFTCGGQLSNWEPKDNAMSEHRRHFPNCPF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN 1 SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW IN TESTIS, BRAIN, AND SKELTPAL MUSCLE.

INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: EXPRESSED PREDOMINANTLY IN THE CYTOPLASM OF THE V-REL-TRANSFORMED CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS50143; BIR_REPEAT_2;
324 324
324 AA; 36567 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
Ā
 68924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36567 MW; SE2B89DEAE3733F3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.4%;
            Repeat.
BIR REPEAT 1.
BIR REPEAT 2.
BIR REPEAT 3.
C3HC4-TYPE.
 ₹.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 228; DE Pred. NO. 3.3e 5; Mismatches
ADF47619650B44A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 13;
,3e-21;
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                                                                                                                                                                                                                                                                                                                      FINGER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                LEVELS
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RESULT OPERORS

TO PROVE OF THE PROVE OF THE
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Best Local Similarity 71.7
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
OSEQOS PRELIMINARY; PRT; 501 AA.
OSEGOS;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
11-JUN-2001 (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Rokaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
MCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9ESFO PRELIMINARY; PRT; 496 AA.
Q9ESFO;
Q1-MAR-2001 (TIEMBLIEL. 16, Created)
Q1-MAR-2001 (TIEMBLIEL. 16, Last sequence update)
Q1-JUN-2001 (TIEMBLIEL. 17, Last annotation updat
INHIBITOR OF APOPTOSIS PROTEIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01282; BIR_REPEAT_1; 1. PROSITE; PS50143; BIR_REPEAT_2; 3. Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Métázoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 LAKAGLYYLGTADKVACFTCGGQLSNWEPKDNAMSEHRRHFPNCPF 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LARAGEYYIGPGDRVACEACGGKLSNWEPKDDAMSEHRRHEPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 Similarity
37; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56117 MW; 9BEF142AAEC5B798 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 185; DB
Pred. No. 1.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 228; DB 13;
Pred. No. 6.2e-21;
5; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11;
.5e-15;
.es 12;
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                                                                                                                                                                                                                                      Dharmarajan
inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 496;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      o
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RESULT
10 PO 15
10 PO 17
10 PO
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Q9EQ04
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Best Local S
Matches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P SEQUENCE FROM N.A.

P STRAIN-WISTAR: TISSUE-OVARY;

C STRAIN-WISTAR: TISSUE-OVARY;

A Lareu R., Bradley C.K., Lacher M., Friis R.R., Dharmaraja

"Cloning, characterization and regulation of an inhibitor of

protein in the rat corpus luteum.";

L Submitted (SEP-2000) to the EmBL/GenBank/DDBJ databases.

C -!- SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.

R EMBL; AF304334; AAG41193.1; ...

R EMBL; AF304334; AAG41193.1; ...

R InterPro; IPR001370; BIR.

R InterPro; IPR001370; BIR.

R Pfam; PF00053; BIR; 3.

R Pfam; PF00053; BIR; 3.

R Pfam; PF000370; STROG STROG; 1.

R SMART; SM0038; BIR; 3.

R SMART; SM0038; BIR; 3.

R SMART; SM00184; RING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.8
Best Local Similarity 71.7
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00653; BIR; 3.
Pfam; PF00097; zf-C3HC4; 1.
SMART; SM00238; BIR; 3.
SMART; SM00184; RING; 1.
PROSITE: PS01282; BIR_REPEAT_1; 1
PROSITE: PS50143; BIR_REPEAT_2; 3
Zinc-finger.
SEQUENCE 501 AA; 56548 MW; 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9EQ04;
                                                                                                                                  O9R015; PRELIMINARY; PRT; 597 AA.

Q9R015; O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NEURONAL APOPPOSIS INHIBITORY PROTEIN.
BIRCLE OR NAIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TEMBLrel. 16, Created)
01-MAR-2001 (TEMBLrel. 16, Last sequence update)
01-UN-2001 (TEMBLRel. 17, Last annotation update)
11HIBITOR OF APOPTOSIS PROTEIN 3.
12HIBITOR OF APOPTOSIS PROTEIN 3.
12HIBIT
AEUkou.
BIRCIE OR NAIr.
Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS01282; BIR_REPEAT_1; PROSITE; PS50143; BIR_REPEAT_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 LASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 LASAGLYYTGIDDQVQCFCCGGKLKNWEPCDRAWSEHRRHFPNCFF 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFPNCPF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LARAGFYYIGPGDRVACFACGGKLSNWEPKDDAMSEHRRHFFNCPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56578 MW; 4863F69FF2E0C8CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.7%;
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Pred. No. 1.5e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 185; DB 11;
Pred. No. 1.5e-15;
1; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω <u>,</u>
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..5e-15;
hes 12;
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inhibitor of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                    Euteleostomi; 
, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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088738
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                                                                                                                                                                               A CONTRACTOR OF THE CONTRACTOR
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Best Local
                                    Query Match
Best Local
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                                    Similarity
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RT inhibitors."

141:1415-1422(1998).

15 Cell Biol. 141:1415-1422(1998).

16 CI- FUNCTION: CAPALYSES THE COVALENT ATTACHMENT OF UBIQUITIN TO OTHER PROTEINS (BY SIMILARITY).

17 CATALYTIC ACTIVITY: ATT + UBIQUITIN + PROTEIN LYSINE - AMP + PYROPHOSHATE + PROTEIN N-UBIQUITYLLYSINE.

18 PATHMAY: SECOND STEP IN UBIQUITYLLYSINE.

19 PATHMAY: SECOND STEP IN UBIQUITYL CONJUGATION.

10 CI- MICCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-

11 CONJUGATION.

10 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

11 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

11 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

11 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

12 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

13 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

14 CI- SIMILARITY: TO UBIQUITIN-CONJUGATING ENZYMES DOMAIN.

15 CHML: Y17267: CAPAG720.1; --

16 CMBL: Y17267: CAPAG720.1; --

17 CMBL: Y17267: CAPAG720.1; --

18 CMBL: Y17267: CAPAG720.1; --

19 CMBL: Y17267: CAPAG720.1; --

10 CMBL: Y17267: CAPAG720.1; --

10 CMBL: Y17267: CAPAG720.1; --

10 CMBL: Y17267: CAPAG720.1; --

11 CMBL: Y17267: CAPAG720.1; --

12 CMBL: Y17267: CAPAG720.1; --

13 CMBL: Y17267: CAPAG720.1; --

14 CMBL: Y17267: CAPAG720.1; --

15 CMBL: Y17267: CAPAG720.1; --

16 CMBL: Y17267: CAPAG720.1; --

17 CMBL: Y17267: CAPAG720.1; --

18 CMBL: Y17267: CAPAG720.1; --

19 CMBL: Y17267: CAPAG720.1; --

10 CMBL: Y17267: CAPAG720.1; --

11 CMBL: Y17267: CAPAG720.1; --

12 CMBL: Y17267: CAPAG720.1; --

13 CMBL: Y17267: CAPAG720.1; --

14 CMBL: Y17267: CAPAG720.1; --

15 CMBL: Y17267: CAPAG720.1; --

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EMBL; AF15493; AAD56765.1; .

HSSP; Ol3490; 10BH.

MGD; MGI:1298220; Bircle.

Interpro; IPR001370; BIR.

Pfam; PF00653; BIR; 3.

SMART; SM00238; BIR; 3.

PROSITE; PS01282; BIR_REPEAT_1; UNKNOWN_2.

PROSITE; PS01287; BIR_REPEAT_2; 3.

SEQUENCE 597 AA; 68322 MW; 4042E36E51A7F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     088738
01-NOV-1998
01-NOV-1998
01-JUN-2001
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MEDILNE-99431676; PubMed-10501978;

Huang S. Scharf J.M., Growney J.D., Endriz

"The mouse Naip gene cluster on Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
UBIQUITIN-CONJUGATING ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98292517; PubMed-9628897;
Hauser H.P., Bardroff M., Pyrowol
"A giant ubiquitin-conjugating en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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{1}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Rodentia;
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Pred. No. 7.4e-10;
4; Mismatches 18
Score
Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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No.
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nosome 13 encodes several dist
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related to
   5.6e-08;
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                                DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h S.;
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QYUENZ
1D QYUENZ
1D QYUENZ
1D QYUENZ
AC QYUENZ
CG12265
GN CG12265
GN CG12265
COS Drosophi
OC Enkaryot
CG Ephydroi
OC Ephydroi
OC Ephydroi
OC Ephydroi
OC Ephydroi
AC Ephydroi
OC Ephydroi
AC Ephydroi
AC Ephydroi
AC Ephydroi
AC ENEATHAINABA
RA Adams M.
RA Adams M.
RA Adams AC MEDLINES
RA ABOLLNES
RA BERSON
RA CHERTY J
RA CHERTY
RA CHERTY
RA CHERTY
RA HEIDIN K.
RA CHERTY
RA CHERTY
RA GIODEK A.
RA HEIDIN K.
RA GIODEK A.
RA HEIDIN K.
RA CHERTY
RA MOUNT S.
RA GIODEK A.
RA FOSIER E.
RA SPIER E.
RA ZEROR
RA CHERTY
RA WILLIAMS
RA ZEROR
RA TIJBASE
DR HESSP. QI
DR PSARTE;
DR SYLERE
DR FISHSP. QI
DR FISHSP. QI
DR FISHSP. QI
DR PSARTE;
PF DR SYLERE
PROSTITE;
SO SEQUENCE
                                        RH SIQUEDE FROM N.A.

RP SEQUED FROM N.A.

RC STRAIN-BERKELEY:

RX MEDLING-20196006; PubMed=10731132;

RX MEDLING-20196006; Scherer S.E., Lil P.W., Hoskins R.A., Galle R.F.,

RA Adams M.D., Celniker S.E., Richards S., Asbburner M., Henderson S.N.,

RA MEDLING-20196006; Rayter E.G., Helt G., Change M., Peiffer B.D.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA MEDLING-20196006; Rayter E.G., Helt G., Welson C.R., Milos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Barris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Howalds C.C., Kraft C., Kravitz S., Killp D. L., Ketchum R.A.,

RA Glodek A., Howalds F., Kaft C., Kravitz S., Killp D. M., Ketchum R.A.,

RA Glodek A., Howalds F., Kaft C., Kravitz S., Killp D. M., Nelson D.L.,

RA Glodek A., Howalds F., Kaft C., McLod M.P., McCherson D.,

RA Glodek A., Gong F., Golfer S., Paller J., Milos J., Milos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CG12265 PROTEIN.
CG12265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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     BIR_REPEAT_2; 1.
; 17455 MW; EE250E3B669EC359 CRC64;
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Query Match 49.3
Best Local Similarity 46.9
Matches 23; Conservative
49.3%;
46.9%;
tive
                                 ; Score 132.5; ; Pred. No. 2.3e; 4; Mismatches
                                             .3e-09;
                                                    DB 5;
                                    indels
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Search completed: January Job time: 1412 sec

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